

CACGCGTCCGCTCTGCTGCTCTAGTGTGACTTTGGCGTCTCAGGTGATCCATGACTTTTAAAGCCATATATATTTCT SEQ ID NO: 1
TACTCCTCTCGGAGTGTGCTTGGCTTTCACTCAGTGTGTTTCTTTTCTTTTCTTTTGGCCTTGGATACCGTTGAGAA
M K V T G F P Q G V T D S M Q C F N 18 SEQ ID NO: 2
TCTA ATG AAA GTC ACG GGC CCT CCC CAG GGA GTT ACA GAC TCC ATG CAA TGC TTC AAT 54
↑SEQ ID NO: 3→
D Q W P L S N T R S S E H I K E V M V E 32
GAT CAG TGG CCT TTA TCT AAC ACC AGG AGC AGC GAG CAC ATA AAA GAG GTC ATG GTT GAG 114
L G K F E R K E F K S S S L Q D G H T K 58
CTG GGC AAG TTT GAA AGG AAG GAG TTT AAA AGT TCC AGT TTG CAA GAT GGA CAT ACA AAA 174
M E E A P T H L N S F L K K E G L T F N 72
ATG CAG GAA GCA CCT ACG CAT CTT AAT TCA TTT CTT AAG AAA GAA GGA TTG ACC TTC AAC 234
R K R K W E L D S Y P I M L W W S P L T 98
AGG AAA AGA AAA TGG GAA TTG GAC AGC TAC CCC ATT ATG CTC TGG TGG TCC CCG CTG ACG 254
G E T G R L G Q C G A D A C F F T I N R 118
GGG CAG ACT GCG AGG TTA GCC CAA TGT GGA GCA GAT GCT TGT TTC TTC ACC ATC AAC CGG 354
T Y L H H H M T K A F L F Y G T D F N I 138
ACC TAC CTC CAT CAT CAC ATG ACC AAA GCA TTC CTC TTC TAT GGT ACT GAC TTT AAC ATA 414
D S L P L P R K A H H D W A V F E E E S 158
GAT AGC TTA CCT CTG CCT CGG AAA GCC CAT CAT GAC TGG GCT GTT TTT CAT GAA GAG TCC 474
P K N N Y K L F H K P V I T L F N Y T A 178
CCG AAA AAC AAT TAT AAG CTC TTT CAT AAA CCA GTG ATT ACC TTG TTC AAC TAC ACT GCC 534
T F S R H S H L P L T T Q Y L E S I E V 198
ACG TTC AGC AGG CAT TCC CAC TTG CCA CTA ACT ACC CAA TAC TTG GAG AGC ATT GAA GTC 594
L K S L R Y L V P L Q S X N K L R K R L 218
CTG AAG TCA CTC CGA TAC CTA GTT CCT TTG CAG TCC AAA AAC AAG CTT AGA AAA AGA CTT 654
A P L V Y V Q S D C D P P S D R D S Y V 238
GCT CCG CTG GTG TAT GTA CAG TCA GAC TGT GAC CCA CCA TCA GAC AGG GAC AGC TAT GTT 714
R E L M T Y I E V D S Y G E C L R N K D 258
CGC GAG CTG ATC ACT TAC ATC GAG GTC GAT TCC TAT GGT GAA TGT TTA CGA AAC AAA GAC 774
L P Q Q L K N P A S M D A D G F Y R I I 278
CTC CCT CAG CAG CTG AAA AAT CCA GCC TCT ATG GAT GCC GAT GGC TTT TAT AGG ATC ATT 834
A Q Y K F I L A F E N A V C D D Y I T E 298
GCA CAG TAT AAG TTT ATC CTA GCT TTT GAG AAT GCA GTT TGT GAT GAC TAC ATC ACT GAG 894
K F W R P L K L G V V P V Y Y G S P S I 318
AAG TTC TGG AGG CCA CTG AAA CTG GGG GTA GTC CCT GTA TAT TAC GGA TCC CCC AGC ATC 954
T D W L P S N K S A I L V S E F S R P R 338
ACA GAC TGG CTT CCA AGT AAC AAA AGT GCT ATT CTT GTA TCA GAA TTT TCT CAC OCC AGG 1014
E L A S Y I R R L D S D D R L Y E A Y V 358
GAA CTG GCA AGT TAC ATC AGA CGA CTG GAT TCT GAT GAC AGA TTG TAT GAG GCC TAT GTA 1074
S W K L K G E I S N Q R L L T A L R E R 378
GAA TGG AAG CTG AAG GGT GAG ATC TCT AAC CAG CGA CTT CTG ACA GCT CTC AGG GAA CGG 1134
K W G V Q D V N Q D N Y I D A F E C M V 398
AAA TGG GGA GTG CAA GAC GTC AAC CAG GAC AAT TAC ATC GAT GCA TTT GAG TGT ATG GTG 1194
C T K V W A N I R L Q E K G L P P K R W 418
TGC ACC AAG CTG TGG GCT AAT ATC AGG CTT CAG GAA AAG GGC TTA CCA CCC AAA AGA TGG 1254
E A E D T H L S C F E P T V F A F S P L 438
GAG GCA GAA GAT ACC CAC CTG AGT TGC CCA GAG CCC ACA GTG TTT GCT TTC TCA CCA CTC 1314

FIG. 1a

```
R  T  P  P  L  S  S  L  R  E  M  W  I  S  S  F  E  Q  S  K  458
CGG ACT CCA CCT TTG AGC TCT TTG CGA GAG ATG TGG ATT TCC AGC TTT GAA CAA TCC AAG 1376

K  E  A  Q  A  L  R  W  L  V  D  R  N  Q  N  F  S  S  Q  E  478
AAA GAA GCC CAG GCA CTA AGG TGG CTG GTT GAT AGG AAT CAA AAC TTT TCA TCT CAA GAG 1434

F  W  G  L  V  F  K  D  *  487
TTT TGG GGC CTA GTA TTC AAG GAC TGA 1461
+SEQ ID NO:37

TTTCAAAATGATCAGAATGAACAGAAAAA
```

FIG. 1b

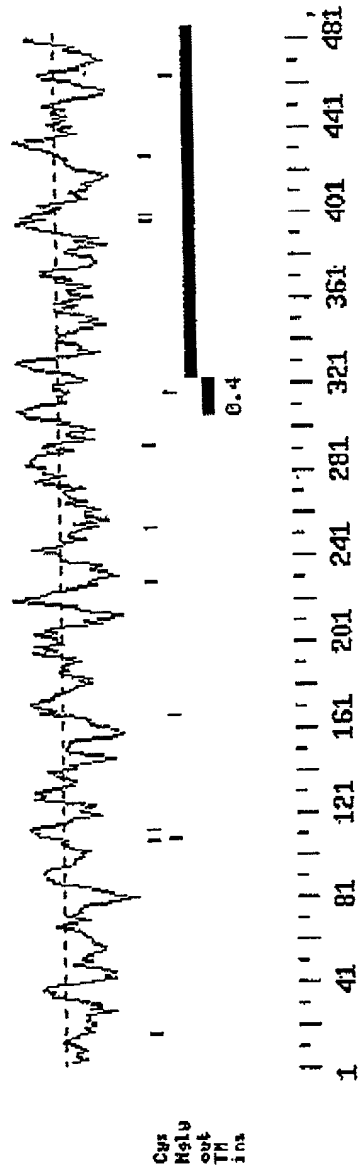


FIG. 2

```

      *->lsdafllrllwrekllGllitvppLllaiaawigleeikewkksplyL      SEQ ID NO:16
      + +  +++ ++e  + +++                +g      e +  +l
80090   35   VMVELGKFERKEF-KSSSLQ-----DGHTKMEEAP-THLN- 67

      SNDHELdVpiLlilSqapqGSrfptleenrillwtwpFndrgaPvppsrc
      + L ++ ++      r   l   +i lw+ p +  g++ + c
80090   68   -----SFLKKEGLTFNRKRKWELDSYPIMLWWSPLT--GETGRLGQC 107

      slsydntarcrltanRsel..esAdavlFNAGHhrDlskgppmdlppeft
      + + c+ t nR  l++      a lF      *D + + +l
80090   108  -----GADACFFTINRTYLhHMTKAFLF---YGTDFNIDSL-PL----- 143

      qvrrarAedaDavllayednaaaaaeaLatdfpRppgQpwVwaSmESPsnsq
      pR+      w  ++ ESP n
80090   144  -----PRKAHHDWAVFHEESPKNN- 162

      RFAVPGFKiNVLNglqilldgyfNwtlSyradsDafhpYGylepltakar
      + ++      +fN t ++ + s      yle
80090   163  -----YKLFHKPVITLFNYTATFSRHSHLPLTTQYLESI----- 196

      kRGFKVqsqvVeaplnlSaKaklaAWVV...SNcntrskRerfykqLkkH
      K + + V+  +  ++ +k  A +V  +S c+  s R  ++++L
80090   197  -EVLKSLRYLVPLQS-KNKLRLKRLAPLVyvqSDCDPPSDRDSYVRELMTY 244

      lqVDvyGrv..anplplksgcsgVe...lietlsqYkFYLaFENSqheD
      + VD yG + +  +lp  + +++      ++      +qYkF LaFEN ++ D
80090   245  IEVDSYGEClrNKDLPPQQLKNPASMDadgFYRIIAQYKFILAFENAVCDD 294

      YvTEKlWkNALqagtiPvVLgPsRavyedFvPpksFihVDDFkSakElAd
      Y+TEK+W+  l  g +Pv+ g s++      ks I V F  ++ElA+
80090   295  YITEKFWR-PLKLGVPVYYG-SPSITDWLPSNKSAILVSEFShPRELAS 342

      YLlyLdknptAYLDmLYENPLNTLDGKAYFYQDLSFKKILDFFKTILEND
      Y++ Ld +
80090   343  YIRRLDSDDL----- 353

      TIYHKYseYFeWRedlrv...rlfswdalrVlEydegfCrvCrlqkapd
      Y Y eW  ++  ++rl++  lr      ++ +  d
80090   354  -----YEAYVEWKLKGEIsnqRLLTA--LR-----ERKWGVQD 384

      llelSryktiplakWFq<-*
      +++  +n+  +F+
80090   385  -----VNQ--DNYIDAFE      395

```

FIG. 3

Query: 89 PI-MLWNS-PLTGETGRLGQCACACFFTINRTYLHHMTKAFIFYGTDFNIDSLPLPRK 146
P+ ++WWS ++ QCG C T R+ + LFYG++ PLPR
Sbjct: 40 PVELVWWSRDMSWNYDVQRQCGIHTCRITNKRS--RRPWARGVLFYGSNIKTGDFPLPRN 97 SEQ ID NO:17

Query: 147 AHHDWAVPHEESPKNKYKLFHKPVITLFNYTATFSRHSHLPLTTQYLESIEVLKSLRYLV 206
H WA+ HEESP+N + +K + F++T+TFSR+S+LPLTT YL S E L S Y V
Sbjct: 98 EHQIWALLHEESPRNTPFVSNKEFLRHFTSTFSRYSNLPLTTMYLPSGEALTSKDYV 157

Query: 207 PLQSKNKLRLAP-LVYVQSDCDPPSDRDSYVRELMTYIEVDSYGECLRNKDLPOQLKN 265
K+K R + +V++QSDCD S R+ YV+EIM ++ +DSYG CLRN+DLP++ K+
Sbjct: 158 TFDGSKYGYRPTSTSVVFLQSDCDTMSGREYVVKELMKHLPIDSYGSLNRDLPERQKD 217

FIG. 4

Query: 221 LVYVQSDCDPPSDRDSYVRELMTYIEVDSYGECLRNKDLPOQLKNPASMDADGFYRIIAQ 280
+ +V S+ +P S R Y ++L +++VD YG R K LPQ +++
Sbjct: 62 VAWVVSNNPNSARVRYYYQLQKHLKVDVYGRSHRGKPLPQ-----GNMETLSR 111 SEQ ID NO:18

Query: 281 YKFLAFENAVCDDYITEKFWR-PLKLGVPVYVYGPSITDW---LPSNKSAILVSEFSH 336
YKF LAFEN++ DYITEK WR L+ G VPV G PS ++ +P + + I V +F
Sbjct: 112 YKFLAFENSMHPDYITEKLRNLAEGAVPVVLG-PSRVNYERFIPPD-AFIVDDFQS 169

Query: 337 PRELASYIRRLDSDRLYEAYVEWKLKGEIS 367
P+ELA Y++ LD + Y Y+ WK + ++
Sbjct: 170 PKELAKYLKELDKNHAAYLKYLRLWKYENPLN 200

FIG. 5

Query: 90 IMLWWSPLTGETGRLGQCGADACFFTINRTYLHHHMTKAF--LFYGTD--FNIDSLPLPR 145
I+LW P +CG C T +R+ H KAF + D ++ + L
Sbjct: 129 ILLWNEPSLVNAPAHVECG---CLVTTSTRS---HNDKAFDAVVISADHPYSFEGLG-GV 180 SEQ ID
NO:19

Query: 146 KAHHD-WAVPHEESPKWNYKLFHKPV--ITL--FNYTATFSRHSPLPLTTQYLESIEVLK 200
K H D +AV+ + P ++ + P+ TL FN T T+ S L T Y + +
Sbjct: 181 KLHPDFYAVYAAKKPLSSTQ--NPLTNFTLPPFNLTMTYRLDSQLIWTDYFSSHNLAR 237

Query: 201 SLRYLVPLQSKNKLRLAPLVY-VQSDCDPPSDRDSYVRELMTYIEVDSYGECLRNKDL 259
L++ SK+ A V ++S+ S L Y+ + + L
Sbjct: 238 RLKWF-RAPSKSFADDMPTTVLRLESEILKKS-----RLAVYLVYEVNEKTLPEPLY 289

Query: 260 PQQLKNPASMADA-DGFYRIIAQYKFI LAFENAVCDDYITEKFWRLKLGVPVVPVYVYGSPI 318
++L+ A +DA D Y F+L FE + C DY+ + + +VPV G ++
Sbjct: 290 MEELRKYADLDAHDNCLGTDHYYHFLIFETSACPDYVPPQMSMAMDKLLVPVVLIGGGNL 349

Query: 319 TDWLPSNKSAILVSEFSPRELASYIRRLDSDRLYEAYVEW----KLKGEISNQRLLTA 374
T+ +PS+ S I +F+ P++L +++ L ++ Y Y W +L+ L +
Sbjct: 350 TNLVPSH-SYISSQDFATPQDLIIHLKDLANNQLEYRRYFWWHYSIYRLRKTSPYCALCS 408

Query: 375 LRERKNGVQDVNQDNY 390
L ++ G +V Q +Y
Sbjct: 409 LIQQSPGGHEVRQRSY 424

FIG. 6

AGCTGCCCTTTGCAGACTCTAACTCCAGCAGC	H N V S F A H L H F A G	12	SEQ ID NO:5
ATG AAT GTG TCC TTT GCT CAC CTC CAC TTT GCC GGA		36	SEQ ID NO:4
↑SEQ ID NO: 6→			
G Y L P S D S Q D W R T I I P A L L V A		32	
GGG TAC CTG CCC TCT GAT TCC CAG GAC TGG AGA ACC ATC ATC CCG GCT CTC TTG GTG GCT		96	
V C L V G F V G N L C V I G I L L H N A		52	
GTG TGC CTG GTG GGC TTC GTG GGA AAC CTG TGT GTG ATT GGC ATC CTC CTC CAC AAT CCT		156	
W K G K P S M I H S L Y L N L S L A D L		72	
TGG AAA GGA AAG CCA TCC ATG ATC CAC TCC CTG ATT CTG AAT CTC AGC CTG GCT GAT CTC		216	
S L L L F S A P I R A T A Y S K S V W D		92	
TCC CTC CTG CTG TTT TCT GCA CCT ATC CGA GCT ACG GCG TAC TCC AAA AGT GTT TGG GAT		276	
L G W F V C K S S D W F I H T C M A A K		112	
CTA GGC TGG TTT GTG TGC AAG TCC TCT GAC TGG TTT ATC CAC ACA TGC AGG GCA GCC AAG		336	
S L T I V V V A K V C F H Y A S D P A K		132	
AGC CTG ACA ATC GTT GTG GTG GCC AAA GTA TGC TTC ATG TAT GCA AGT GAC CCA GCC AAG		396	
Q V S I H N Y T I W S V L V A I W T V A		152	
CAA GTG AGT ATC CAC AAC TAC ACC ATC TGG TCA GTG CTG GTG GCC ATC TGG ACT GTG GCT		456	
S L L P L F E W F F S T I R H H E G V E		172	
AGC CTG TTA CCC CTG CCC GAA TGG TTC TTT AGC ACC ATC AGG CAT CAT GAA GGT GTG GAA		516	
M C L V D V P A V A E E F M S H F G K L		192	
ATG TGC CTC GTG GAT GTA CCA GCT GTG GCT GAA GAG TTT ATG TCG ATG TTT GGT AAG CTC		576	
Y P L L A F G L F L F F A S F Y F W R A		212	
TAC CCA CTC CTG GCA TTT GGC CTT CCA TTA TTT TTT GCC AGC TTT TAT TTC TGG AGA GCT		636	
Y D Q C K K R G T K T Q N L R N Q I R S		232	
TAT GAC CAA TGT AAA AAA CCA GGA ACT AAG ACT CAA AAT CTT AGA AAC CAG ATA CGC TCA		696	
K Q V T V M L L S I A I I S A L L W L P		252	
AAG CAA GTC ACA GTG ATG CTG CTG AGC ATT GCC ATC ATC TCT GCT CTC TTG TGG CTC CCC		756	
E W V A W L W V W H L K A A G P A P P Q		272	
GAA TGG GTA CCT TGG CTG TGG GTA TGG CAT CTG AAG GCT GCA GGC CCG GCC CCA CCA CAA		816	
G F I A L S Q V L M F S I S S A N P L I		292	
GGT TTC ATA GGC CTG TCT CAA GTC TTG ATG TTT TCC ATC TCT TCA GCA AAT CCT CTC ATT		876	
F L V M S E E F R E G L K G V W K W H I		312	
TTT CTT GTG ATG TCG GAA GAG TTC AGG GAA GGC TTG AAA GGT GTA TGG AAA TGG ATG ATA		936	
T K K P P T V S E S Q E T P A G N S E G		332	
ACC AAA AAA CCT CCA ACT GTC TCA GAG TCT CAG GAA ACA CCA GCT GGC AAC TCA GAG GGT		996	
L P D K V P S P E S P A S I P E K E K P		352	
CTT CCT GAC AAG GTC CCA TCT CCA GAA TCC CCA GCA TCC ATA CCA GAA AAA GAG AAA CCC		1056	
S S E S S G K G K T E K A E I P I L P D		372	
AGC TCT CCC TCC TCT GGC AAA GGG AAA ACT GAG AAG GCA GAG ATT CCC ATC CTT CCT GAC		1116	
V E Q F W H E R D T V P S V Q L K S T N		392	
GTA GAG CAG TTT TGG CAT GAG AGG GAC ACA GTC CCT TCT GTA CAA TTG AAG AGC ACC AAC		1176	
P T D C G S S G N S A W Y R K T E K S A		412	
CCT ACA GAT TGT GGT AGC TCA CGT AAC TCA GCG TCG TAC CGC AAA ACT GAA AAA TCA GCA		1236	
C C P K T E I H S T F Y F Q I L L L A Y		432	
TGT TGC CCT AAG ACG GAA ATC CAT TCA ACA TTC TAC TTC CAG ATA CTG CTT CTA GCA ATT		1296	
H R N R N H I S R F S T K Q L L L G L Q		452	
CAC AGA AAC AGA AAC CAC ATC TCA CGT TTC TCA ACT AAA CAA CTG CTT TTA GGA CTG CAG		1356	

FIG. 7a

H K F R F S V F E *
CAC AAG TTC AGA TTT TCT GTC TTT CCT TAA
←SEQ ID NO:6↑
GTC

462
1386

FIG. 7b

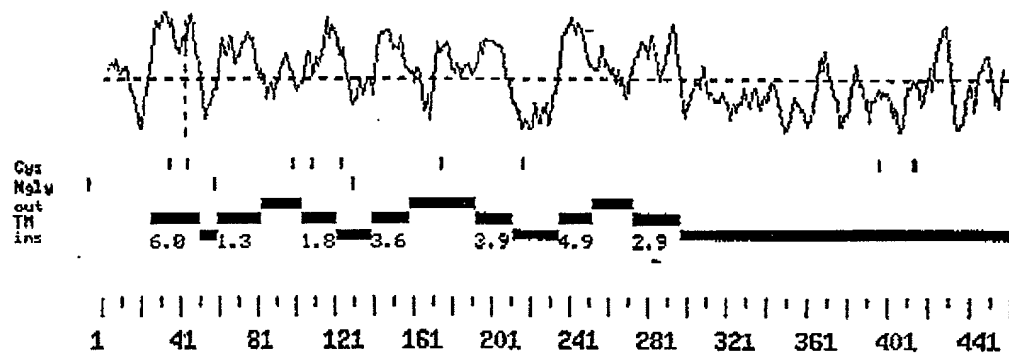


FIG. 8

```

      *->GNILVilvilttkklr..tptnifilNLavADLLfilitlppwalyyl  seq ID NO:20
      GNl Vi ++l +      +++++ + +ilNL++ADL +ll+ p+ +++++
52874   40  GNLCVIGILLHNAWKgkpSMIHSLILNLSLADLSLLLFSAPIRATAY 86

      vggssedWpfGsalCklvtaldvvnmyaSillLtaIS<-*
      + W +G ++Ck +  ++ ++m a l++++ +
52874   87 SK--SVWDLGWfVCKSSDNFIHTCMAAKSLTIVVVA 120

```

FIG. 9a

```

      *->kvvillvWvlalllsIppllfswvktveegngtlnvntvClidfpe  seq ID NO:21
      + v++++W++a ll lP +fs+ +++e+ +      +Cl+d p
52874   142  WSVLVAIWTVASLLPLPEWFFSTIRHHEGVE-----MCLVDVPA 180

      estasvstwlreyvllstlvGfllPllvilvcYtrilrtlr.....
      ++      +++++ + l l++F lPl++ +++ +r +      +++++++
52874   181  VA---EEFMSMFGKLYPLLAfGLPLFFASFYFWRAYDQCKKrgtktgnl 226

      .....kaaktllvvvvvFvlCWlPyfivllldtlc.lsiimsstCele
      +++ +++++ +ll + ++ +l+WlP +++l+ ++ + +
52874   227  rnqirskQVTVMLLSIAIISALLWLPWVAVLWVWHLKAAGP----- 268

      rvlptallvtlwLayvNscINPiIY<-*
      + ++ ++ ++ +L ++ S' NP+I
52874   269 APPQGFIALSQVLMFSSISANPLIF 293

```

FIG 9b

```

Query:  253 EWVAVLW-VWHLKAAGPAPPQGFIALSQVLMFSSISANFLIFLVMSEEFREGLKGVW--- 308
      EW WL+ V+H      F +S VL + S+ NP+++ +MS FRE K V
Sbjct:  12 EWTEWLYDVYHY-----FHMVSGVLfYLSSAINPILYNLMShRFREAPKNVLSSL 61  seq ID NO:22

Query:  309 --KWMITKKP-PTVS 320
      +W      KP P+ S
Sbjct:  62 CKQWHSRHKPRPSFS 76

```

FIG. 10

Query: 208 YFWRAYDQC-KKRGTKTQNLNRNQIRSKQVTVMXXXXXXXXXXXXXWLPBWVAVLWVWHLKAA 266
YF C +KR +T+ + R+ +VT+M WLP W+ W ++A
Sbjct: 160 YFKIILKMCQRKQMOTKRTATKRTTKVTIMGLAIVISYTHCWLPPFWIVQ---WSIEAN 216 SEQ ID NO:23
Query: 267 GPAPPQGFIALSQVLMFSI----SSANPLIFLVMSEEFREGLKGVWKMITKKP 316
+ + F++ S+ANP +++ +S+ F+ K + K + T KP
Sbjct: 217 LFEKSKYLLFCCTHFAFALQYINSAANPFLYVFLSDSFQ---KNIQKLLRTAKP 267

FIG. 11

Query: 16 PSDSQDWR--TIIPALL---VAVCLVGFVGNLCVIGILLHNAWKGPSPMI-HXXXXXXXXX 69
PSD+ + T++ +L + L+ F N+ + G++ W K +++ H
Sbjct: 115 PSDAPETYSDTVLSVVLGFYALLLLIAFASNILLAGVIKKYRWGMKQALLFHLCTVGALL 174 SEQ ID NO:24
Query: 70 XXXXXXXXXAP----IRATAYSKSVWDLGNFVCKSSDWFHTCMAAKSLTIVVVAKVCF- 124
A ++ S +V L F + W H A + ++ +A CF
Sbjct: 175 SITNTLHLLASGYHLLKQRNSSTV--LQSFALIA--WVDHFIGFALLIFVMYLAIFCFK 230
Query: 125 MYASDPAKQVSI-HNYTIWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPAVAE 183
Y ++ + + +Y +++V ++ W +A L+ PF H + C+ V AV+
Sbjct: 231 FYWNNKIRSIENGRSYVLYAV-ISTWVIAFLIAGFTAFFQCDSHINSQDQCIQIVCAVSN 289
Query: 184 EFMSMFGKL 192
F ++F +L
Sbjct: 290 IFSAIFTEL 298

FIG. 12

TACTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTCTAGAAATTCAGCGGCCGCTGAATTCTAGGCTGCTCTGGGCTT SEQ ID NO:7
TGCTAGCCGGCTCTGCACCTCCAGAGCCGCTGGGCACGCCCTCAGCTGCTCCATCGCCTCACTTTCCAGGCTCGCG

CCCGAAGCAGAGCCATGAGAACCCAGGGTGCCCTGGCGAGCCGCTAGCGCC M G F G E A L 7 SEQ ID NO:8
ATG GGC CCC GGC GAG GCG CTG 21
↑SEQ ID NO: 9↓

L A G L L V M V L A V A L L S N A L V L 27
CTG GCG GGT CTT CTG CTG ATG GTA CTG GCC GTG-GCG CTG CTA TCC AAC GCA CTG GTG CTG 81

L C C A Y S A E L R T R A S G V L L V N 47
CTT TGT TGC GCC TAC AGC GGT GAG CTC CGT ACT CGA GCC TCA GGC GTC CTC CTG GTG AAT 141

L S L G H L L L A A L D M P F T L L G V 67
CTG TCG CTG GGC CAC CTG CTG CTG GCG GCG CTG GAC ATG CCC TTC ACG CTG CTC GGT GTG 201

M R G R T P S A P G A C Q V I G F L D T 87
ATG CGC GGG CGG ACA CCG TCG GCG CCC GGC GCA TGC CAA GTC ATT GGC TTC CTG GAC ACC 261

F L A S N A A L S V A A L S A D Q W L A 107
TTC CTG GCG TCC AAC GCG GCG CTG AGC GTG GCG GCG CTG AGC GCA GAC CAG TGG CTG GCA 321

V G F P L R Y A G R L R P R Y A G L L L 127
GTG GGC TTC CCA CTG CGC TAC GCC GGA CGC CTG CGA CCG CGC TAT GCC GGC CTG CTG CTG 381

G C A W G Q S L A F S G A A L G C S W L 147
GGC TGT GCC TGG GGA CAG TCG CTG GCC TTC TCA GGC GCT GCA CTT GGC TGC TCG TGG CTT 441

G Y S S A F A S C S L R L P P E P E R P 167
GGC TAC AGC AGC GCC TTC GCG TCC TGT TCG CTG CGC CTG CCG CCC GAG CCT GAG CGT CCG 501

R F A A F T A T L H A V G F V L P L A V 187
CGC TTC GCA GCC TTC ACC GCC ACG CTC CAT GCC GTG GGC TTC GTG CTG CCG CTG GCG GTG 561

L C L T S L Q V H R V A R S H C Q R M D 207
CTC TGC CTC ACC TCG CTC CAG GTG CAC CGG GTG GCA CGC AGC CAC TGC CAG CGC ATG GAC 621

T V T M K A L A L L A D L H P S V R Q R 227
ACT GTC ACC ATG AAG GCG CTC GCG CTG CTC GCC GAC CTG CAC CCC AGT GTG CGG CAG CGC 681

C L I Q Q K R R R H R A T R K I G I A I 247
TGC CTC ATC CAG CAG AAG CGG CGC CGC CAC CGC GCC ACC AGG AAG ATT GGC ATT GCT ATT 741

A T F L I C F A P Y V M T R L A E L V P 267
GCG ACC TTC CTC ATC TGC TTT GCC CCG TAT GTC ATG ACC AGG CTG GCG GAG CTC GTG CCC 801

F V T V N A Q W G I L S K C L T Y S X A 287
TTC GTC ACC GTG AAC GCC CAG TGG GGC ATC CTC AGC AAG TGC CTG ACC TAC AGC AAG GCG 861

V A D F F T Y S L L R R P F R Q V L A G 307
GTG GCC GAC CCG TTC ACG TAC TCT CTG CTC CGC CGG CCG TTC CGC CAA GTC CTG GCC GGC 921

M V H R L L X R T P R P A S T H D S S L 327
ATG GTG CAC CGG CTG CTG AAG AGA ACC CCG CGC CCA GCA TCC ACC CAT GAC AGC TCT CTG 981

D V A G H V H Q L L K R T P R P A S T H 347
GAT GTG GCC GGC ATG GTG CAC CAG CTG CTG AAG AGA ACC CCG CGC CCA GCG TCC ACC CAC 1041

N G S V D T E N D S C L Q Q T H * 364
AAC GGC TCT GTG GAC ACA GAG AAT GAT TCC TGC CTG CAG CAG ACA CAC TGA 1092

GGGCCTGGCAGGGCTCATCGCCCCACCTTCTAAGAAGCCCTGTGGAAGA <SEQ ID NO:9T

FIG. 13

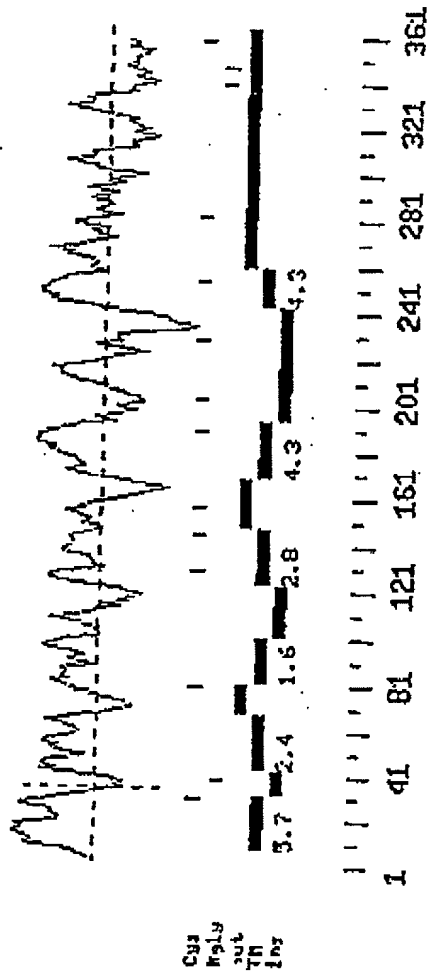


FIG. 14

```
*->GNILVilvilitrkklr.tptnifiINLAVADLLfltlppwalylv seq ID NO:25  
N+LV+l +++ lr++++ ++NL++ LL++++ +p++l+ ++  
52880      22   SNALVLCCAYSaelRtRASGVllVNLSLGHILLAAldMPFTLLGVM 68  
  
ggssdWpfGsaiCklvtaldvvnmYaSillLtaISIDRYIAIvhPlryrr  
g * p + C + ++ld++ l+ +aS D +!A+ Plry  
52880      69 RG--RTPSAPGACQVIgfLDTFLaSNaaLSVAALSAdQLavGFPLRYAG 116  
  
rrtsprrrAkvvilivWvlalillsIpplfswvkTveegngltInvnvtvCl  
x + pr A *****W +l+s l+++ ++ +C+  
52880     117 RLR-PRYagLLLGCawQSlaFSGAA-LGCSWLGYSSA-----FASCS 157  
  
idfpeestasvwstwlrsyvlStlgFlPllvilvcYtriltlr....  
+ p e+ ++ +++ ++ vgF+lPl v++ + +++ r+r++ +  
52880     158 LRLPEEP--ERPREFAATLHAvgfvLPavlLCITSLQVHRVARshcq 204  
  
.....kaaktllvvvvFvlCW  
* ++ + + + + + + + + + + + + + + F++C+  
52880     205 zmdtvtkalalladlhpsvrqrcliqqkrrrhRATRKiGiAiAtFLICF 254  
  
lpfiivilldtlc.lsiimssetCelervlptallvtlwLAYvNsclNPii  
+Py + l + V + +++ +Ly+ ++ +P+  
52880     255 APYvmTRLAEIVPfVT-----VNAQGILSKCLTYskAvADPF 293  
  
Y<-*  
Y  
52880    294 Y       294
```

FIG. 15

```

Query:      134 SLAFSGAALGCSWLGYSSAFASCSXXXXXXXXXXXXFAAFTATLHAVGVFLPLAVLCLTSL 193
             +L F  AL  SWLG+  +ASC+                FA FT+  HA+  F+L  VLC T L
Sbjct:      2  ALTFPATALALSWLGFHQLYASCTLCSRRPDERLRFAVFTSAFHALSPLL SFIVLCFTYL 61  SEQ ID NO:26

Query:      194 QVHRVARSHCQRMETVTMKALALLADLHPSVRQRLIQKKRRRRHRATRKGIGIAIATFLIC 253
             +V +VAR HC+R+D +TM+ L LL D+HPSVR+RCL +QKKRR RAT+KI  I TFL+C
Sbjct:      62 KVLKVARFHCKRIDVITMQTLVLVLDIHPSVRERCLEEQRKRQRATKIKISTFIQTFFLVC 121

Query:      254 FAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLRRPFRQVLAMVHRL 313
             FAPYV+TRL EL      +++ WG+LSKCL YSKA +DPF YSLLR  +R+      +++R+
Sbjct:      122 FAPYVITRLVELFSTAPIDSHWGVLSKCLAYSKAASDPFVYSLLRHQYRRSCKELLNRIF 181

Query:      314 KR 315
             R
Sbjct:      182 NR 183

```

FIG. 16

Query: 175 TLHAVGFVLPLAVL--CLTS--LQVHRVARSHCQRM DVTM KALALLADLHPSVRQRC LI 230
TL VGF++P V+ C L VH + + D + A +
Sbjct: 28 TLFI VGFMI PCLVIIVCYACIPLTVHH-QKKKIRNHDNFQIAAAKGSSSSGGGSYMTTTC 86 SEQ ID NO:27

Query: 231 QQKRRRHRATRK-IGIAIATFLICFAPY---VMTRLAELVPFVTVNAQ---WGILSKCL 282
+K R R T K + + F IC+ P V+ R+ + N W I S L
Sbjct: 87 TRKAREDRKTTKMLMVFLCFAICYLPISILNVLKRVEGFMFRHSEDNESVYWWHIFSHWL 146

Query: 283 TYSKAVADPFTYSLLRRPFRQVLAGMVHRLKRTPRPAS 321
Y+ + +P Y+ + +R+ + LLK P S
Sbjct: 147 VYANSCINPIIYNFMNGKYRKAY-WKIFALLKFWGEPLS 184

FIG. 17

Query: 171 AFTATLHAVGFVLPLAVL-----CLTSLQVHRVARSHCQRM DVTM KALALLADLHPSVR 225
A+ L F +P +V+ C+ + H R H D++ + ++ L L R
Sbjct: 24 AYVVM LVVAVFFIFBSVMLYSYMCILNTVRHNAVRIH-NHPDSLCLSQVSKLG-IMSLQR 81 SEQ ID NO:28

Query: 226 QRCLIQKRRRHRATRKIGIAIATFLICFAPY-VMTRLAELVPFVTVNAQWGILSKC--- 281
+ + RA I I F +C+ P+ V + L+ + +S C
Sbjct: 82 PHQMSVDMSEKTRAF TTTILILFVGFSLCWLPHSVSYLSLVFSKHFFYQHNFFEISTCVLW 141

Query: 282 LTYSKAVADPFTYSLLRRPFRQVLAGMVHRLKRTPR-PAST 322
L Y K+V +P Y + FR+ M+ + K P+ P T
Sbjct: 142 LCYLKSVFNPIIYC WRIKKFREACLEMPKTFKILPQVPGRT 183

FIG. 18

Query: 221 HPSVRQRC LIQQKRRRHRATRKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSK 280
H ++ CL+QQK R+ A+ G+A A +P R F W L
Sbjct: 7 HKIIKAACLVQQK RQEF L ASVARGVAPAD-----SPEAPRR-----SFAGGTWDWEYLG- 55 SEQ ID NO:29

Query: 281 CLTYSKAVADPFTYSLLRRPFRQVLAGMVHRLKRTPRPASTHSSLDV 329
+ A+ F Y RR RQ G VH LL P P +S+LD+
Sbjct: 56 -FASPEEYAE-FQY---RRRHRQRRRGDVHSLLSNPPDPDEPSESTLDI 99

FIG. 19

CTGTGACTTTAAGTATTTCTAAGGCGCAGAGCAATGGGAGGTGGAGAACTGCTGGGTTGCAGGTGACACTATAACGTAGA SEQ ID NO:10

TCATGCCTCCTATTTCCATGCAGGACCTCCAGCCCTGAAGCAACATCAGTGACAGACATCASTGGCAGA H 1 SEQ ID NO:11
ATG 3
↑SEQ ID NO:12→

A S R Y V A V G M I L S Q T V V G V L G 21
GCC TCC CGG TAT GTG GCA GTG GGA ATG ATC TTA TCA CAG ACC GTG GTG GGA GTC CTG GGG 63

S F S V L L H Y L S F Y C T G C R L R S 41
AGC TTC TCT GTT CTT CTC CAT TAT CTC TCC TTT TAC TGC ACT GGG TGC AGG TTA AGG TCC 123

T D L I V K H L I V A N F L A L R C K G 61
ACA GAT TTG ATT GTT AAG CAC CTG ATT GTA GCC AAC TTC TTA GCT CTC CGC TGT AAA GGA 183

V P Q T M A A F G V R Y F L N A L G C K 81
GTC CCC CAG ACA ATG GCA GCT TTT GGG GTT AGA TAT TTT CTC AAT GCT CTT GGG TGC AAA 243

L V F Y L H R V G R G V S I G T T C L L 101
CTT GTT TTC TAT CTC CAT AGA GTG GGC AGG GGA GTG TCC ATT GGC ACC ACC TGC CTC TTG 303

S V P Q V I T V S S R K S R W A K L K E 121
AGT GTC TTC CAG GTG ATC ACG GTC AGC TCC AGG AAA TCC AGG TGG GCA AAA CTT AAA GAG 363

K A P K H V G F S V L L C W I V C M L V 141
AAA GCC CCC AAG CAT GTT GGC TTT TCT GTT CTC CTG TGC TGG ATC GTG TGC ATG TTG GTA 423

N I I F P K Y V A G K W N Y T N I T V N 161
AAC ATC ATC TTT CCC ATG TAT GTG GCT GGC AAA TGG AAC TAC ACA AAC ATC ACA GTG AAC 483

E D L G Y C S G G G N N K I A Q T L R A 181
GAG GAT TTG GGA TAC TGT TCT GGG GGA GGC AAC AAC AAA ATC GCA CAG ACA CTG CGT GCA 543

M L L S F P D V L C L G L M F W V S S S 201
ATG TTG TTA TCA TTC CCT GAT GTG TTG TGT CTG GGG CTC ATG TTC TGG GTC AGC AGC TCC 603

M V C I L H R H K Q R V Q H I D R S D L 221
ATG GTT TGC ATA CTG CAC AGG CAC AAG CAG CGG GTC CAG CAC ATT GAT AGG AGC GAT CTC 663

S P R A S P E H R A T Q S I L I L V S T 241
TCC CCC AGA GCC TCC CCA GAG AAC AGA GCT ACG CAG AGC ATC CTC ATC CTG GTG AGC ACC 723

F V S S Y T L S C L F Q V C M A L L D N 261
TTT GTG TCT TCT TAC ACT CTC TCC TGC CTT TTC CAA GTT TGT ATG GCT CTT TTG GAT AAT 783

P N S L L V N T S A L M S V C F F T L S 281
CCC AAT AGT TTA CTG GTG AAC ACT TCA GCC TTA ATG AGT GTA TGT TTC CCA ACT CTC AGC 843

P F V L H S C D F S V Y R F C F A W K R 301
CCC TTT GTT CTC ATG AGC TGT GAC CCC AGT GTA TAC AGG TTT TGT TTT GCC TGG AAA AGA 903

TGA 302
←SEQ ID NO:12↑ 906

CAAGATCTCCTAACCTCATATAACATGTACATTGTATATATTTGCTCATGGTTCAATTGATGACTTACTCTTCTGTG

CCGCACCTGCCCGGGCGGCGCTCGAGCCCTATAGTGAGTA

FIG. 20

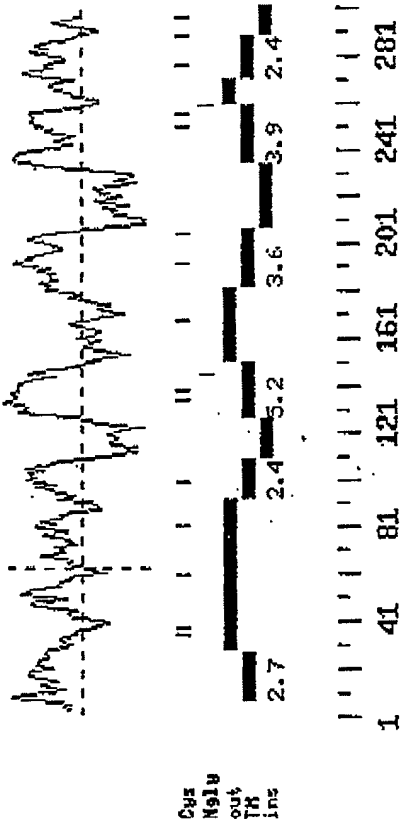


FIG. 21

```

-->llPlvlvcYtrIlrtr.....kaaktl SEQ ID NO:30
+i+l ++ + + ++++l+++++ ++ ++++ +++ +++++a+ +
63497 189 VLCLGLMFVSSSMVCILHrhkqrqhidsdlspaspenRATQSI 235

lvvvvfv<-*
l++v++fv
63497 236 LILVSTFV 243

```

FIG. 22

```

Query: 36 GCRLRSTDLIVKHLIVANFLALRCKGVPTMAAFGVRYFLNALGCKLVFYLHEVGRGVSI 95
      G R R TDL + L + + + L G TM F + CK + YLHR+ RG+S+
Sbjct: 5 GHRSEPTDLFIGHLSLVHLMLLTMGFLATMDMFMSWGRWDDTCKSLIYLRLLRGLSL 64 SEQ ID NO:31

Query: 96 GTICLLSVFQVITVSSRSRMAKLKEKAPKHVGFSVLLCWIVCGLVNIIPPMYVAGKWNV 155
      TTCLL+VFQ IT+S R S AK K K+P H+ + L W++ M + + + N
Sbjct: 65 CTICLLNVFOAITLSFRSSCLAKFKHKSPHHSCTFLFLWVLYMSFSSEHLLLSIATPNL 124

Query: 156 TNITVNEDLGYSGGGNNKLAQTLRAMLLSFDPVCLGLMFVSSSMVCILHrhkqrqh 215
      T+ CS + Q++ + LL+ DV +GLM S MV +L RH+++ QH
Sbjct: 125 TSNDFMYVTQSCSILPMSYSMSMFSTLLAIRDVTFLGLMVLSSGYMVALLCPHRKQAQH 184

Query: 216 IDRSDLSPRASPENRATQSILILVSTF-VSSYTL-SCLFQVCMALLDNFNSLLVNTSALM 273
      + + LSP+ASPE KAT++IL+L+S+F V Y S +F D P + ++
Sbjct: 185 LHSTSLSPKASPEQPATRITILMLMSSFFVLMYIFDSIVFCSRTMFKDGPTFYCIQI--IV 242

Query: 274 SVCFPTLSPFVLMSCDPSVYRF 295
      S + T+SPFV + + + +F
Sbjct: 243 SHSYATVSPFVFICTEXHIVKF 264

```

FIG. 23

TCGCCAGGCGAGACAGGAACCTCTTCCCTTCTCTGTGTGTCAGGATCGCAGAAAGTATGTCCCTTCTCTCACC ATG
S W L S S S Q G V V L T A Y H P S G K D
AGC TGG CTC TCC AGT TCC CAG GGA GTG GTA CTA ACA GCC TAC CAC CCC AGC GGC AAG GAC
Q R V G N S F A K A G E E A T S S R R Y
CAG GCC GTC GGG AAC AGC CAT GCA AAG GCA GGG GAG GAA GCC ACC TCG AGT CGC AGA TAT
G Q Y T M N Q E S T T I K V M E K P P F
GGC CAG TAC ACT ATG AAC CAG GAA AGC ACC ACC ATC AAA GTT ATG GAG AAG CCT CCA TTT
D R S I S Q D S L D E L S M E D Y W I E
GAT CGA TCA ATT TCC CAG GAT TCT TTG GAT GAA CTA TCT ATG GAA GAC TAT TGG ATA GAA
L E N I K K S S E N S Q E D Q E V V V V
CTA GAA AAC ATC AAG AAA TCT AGT GAA AAC AGC CAA GAA GAT CAA GAG GTG GTT GTT GTC
K E P D E G E L E E E W L K E A G L S N
AAA GAG CCT GAT GAG GGA GAA TTG GAA GAA GAG TGG CTT AAA GAG GCC GGT TTA TCC AAT
L F G E S A G D P Q E S I V F L S T L T
CTC TTC GGA GAG TCT GCT GGA GAT CCA CAG GAA AGC ATT GTG TTT TTA TCA ACA TTG ACG
P T Q A A A V Q K R V E T V S Q T L R K
CGG ACC CAG GCA GCA GCA GTT CAG AAG CGA GTA GAG ACG GTC TCC CAG ACC TTG AGA AAA
K N K Q Y Q I P D V R D I F A Q Q R E S
AAA AAC AAA CAG TAC CAG ATT CCT GAC GTC AGA GAC ATA TTT GCT CAA CAG AGA GAA TCA
K E T A P G G T E S Q S L R T N E N K Y
AAA GAA ACA GCT CCA GGT GGC ACT GAA TCG CAG TCA CTT AGA ACA AAT GAA AAC AAA TAC
Q G R D D E A S N L V G B E K L I P F E
CAA GGA AGA GAT GAC GAG GCA TCT AAC CTT GTT GGT CAA GAG AAG CTG ATC CCA CCT GAG
E T P A P E T D I N L E V S F A E Q A L
GAG ACG CCT GCC CCT GAA ACA GAC ATC AAC CTG CAG GTA TCA TTT GCC GAG CAA GCA CTC
N Q K E S S K E K I Q K S K G D D A T L
AAT CAG AAA GAG AGC TCC AAG GAG AAA ATC CAG AAG AGC AAA GGC GAT GAT GCC ACA TTA
P S F R L P K D K T G T T R I G D L A P
CCT AGT TTC AGA TTG CCA AAA GAC AAA ACG GGT ACC ACA AGG ATT GGT GAC CTC GCA CCC
Q D M K K V C E L A L I E L T A L Y D V
CAG GAC ATG AAG AAA GTT TGC CAT TTA GCC CTA ATT GAG CTG ACT GCC CTC TAT GAT GTA
L G I E L K Q Q K A V K I K T K D S G L
TTG GGT ATT GAG CTG AAA CAA CAA AAA CCT GTG AAA ATC AAA ACA AAA GAT TCT GGT CTT
F C V P L T A L L E Q D Q R K V P G H R
TTT TGC GTT CCA TTG ACA GCG CTA TTA GAA CAA GAT CAG AGG AAA GTA CCA GGA ATG CGA
I P L I F Q K L I S R I E E R G L E T E
ATA CCC TTG ATC TTT CAA AAA CTG AAT TCT CGA ATT GAA GAG AGA GGT TTG GAA ACA GAA
G L L R I P G A A I R I K N L C Q E L E
GGC CTC TTA CCG ATC CCT GGA GCT GCC ATT AGA ATC AAG AAT CTT TGC CAA GAA CTA GAA
A K F Y E G T F N W E S V K Q H D A A S
GCA AAG TTT TAT GAA GGG ACT TTT AAT TGG GAA AGT GTC AAA CAG CAT CAT GCC GCC AGC
L L K L F I R E L P Q P L L S V E Y L K
CTG CTG AAG CTC TTC ATT CGG GAG TTG CCC CAG CCA CTC CTC AGT GTG GAG TAT CTC AAA
A P Q A V Q N L P T K K Q Q L Q A L N L
GCC TTT CAG GCT GTC CAG AAT CTT CCA ACC AAG AAG CAG CAA CTA CAG GCT TTG AAC CTT

FIG. 24a

L	V	I	L	L	P	D	A	N	R	D	T	L	K	A	L	L	E	F	L	461
CTT	GTC	ATC	CTC	CTA	CCT	GAT	GCA	AAC	AGG	GAC	ACA	CTG	AAG	GCC	CTT	CTT	GAA	TTT	CTC	1383
Q	R	V	I	D	N	K	E	K	N	K	M	T	V	M	N	V	A	M	V	481
CAA	AGA	GTA	ATA	GAT	AAT	AAA	GAA	AAA	AAT	AAA	ATG	ACA	GTC	ATG	AAT	GTA	GCA	ATG	GTC	1443
M	A	P	N	L	F	M	C	H	A	L	G	L	K	S	S	E	Q	R	E	501
ATG	GCC	CCG	AAT	CTC	TTT	ATG	TGT	CAT	GCA	TTG	GGA	TTG	AAG	TCC	AGT	GGA	CAG	CGA	GAA	1503
F	V	M	A	A	C	T	A	N	T	M	H	L	L	I	K	Y	Q	K	L	521
TTT	GTA	ATG	GCA	GCT	GGG	ACA	GCA	AAT	ACC	ATG	CAC	TTA	TTG	ATT	AAG	TAC	CAA	AAA	CTT	1563
L	W	T	I	F	K	F	I	V	N	Q	V	R	K	Q	N	T	E	N	H	541
CTG	TGG	ACA	ATT	CCC	AAG	TTT	ATT	GTA	AAC	CAA	GTG	AGG	AAG	CAA	AAC	ACG	GAA	AAT	CAT	1623
K	K	D	K	R	A	M	K	K	L	L	K	K	M	A	Y	D	R	E	K	561
AAA	AAG	GAT	AAA	AGA	GCC	ATG	AAG	AAA	TTG	CTG	AAG	AAA	ATG	GCT	TAT	GAC	CGA	GAA	AAA	1683
Y	E	K	Q	D	K	S	T	N	D	A	D	V	P	Q	G	V	I	R	V	581
TAT	GAA	AAG	CAA	GAT	AAG	AGT	ACA	AAT	GAT	GCT	GAC	GTT	CCT	CAG	GGA	GTG	ATT	CGA	GTG	1743
Q	A	P	H	L	S	K	V	S	M	A	I	Q	L	T	E	E	L	K	A	601
CAA	GCT	CCC	CAT	CTT	TGG	AAA	GTT	TCC	ATG	GCA	ATA	CAG	CTA	ACT	GAA	GAA	CTA	AAA	GCC	1803
S	D	V	L	A	R	F	L	S	Q	E	S	G	V	A	Q	T	L	K	K	621
AGT	GAT	GTA	CTT	GCC	AGG	TTT	CTC	AGC	CAA	GAA	AGT	GGG	GTT	GCC	CAG	ACT	CTC	AAG	AAA	1863
G	E	V	F	L	Y	E	T	G	G	N	I	G	E	R	C	L	D	D	D	641
GGA	GAA	GTT	TTT	TTG	TAT	GAA	ATT	GGA	GGA	AAT	ATT	GGG	GAA	CGC	TGC	CTT	GAT	GAT	GAC	1923
T	Y	M	R	D	L	Y	Q	L	N	E	N	A	E	W	V	I	K	S	K	661
ACT	TAC	ATG	AAG	GAT	TTA	TAT	CAG	CTT	AAC	CCA	ART	GCT	GAG	TGG	GTT	ATA	AAG	TCA	AAG	1983
P	L	*																		664
CCA	TTG	TAG																		1992

←SEQ ID NO:15 ↑

AAGACTTAAACAAGCTGCAGATAACCATGTGGACTTCTGTCTAATTCCTTGCTGAGTCAAGAGTGTAAATAAAGAAATG
 GCAGGACTCATATTATTTCAGTTGTATCCCAAGTATTTAAAAATGACTCTCTTAAGCCTTAAAGGTCTAGATTGTGCT
 GCTGCCAGAAATTATATTATTATTATTATTAATGTTATTATTAGAAAAAAATTTCTGGAGTGAAGTAAAGAGGCTTAAT
 AGTTTGTGGCCAGTTTTCATATGCTCTGTGAATGTGTCCAGATGTGACATAGTTTCTTTTATATATGTGGAAATG
 TCTTCTCTCCCATCTTTCTCTTAAATCATATATACTGTAAATATATGCTCTCTCAGCTCTATTACCTCTCCATC
 TACCCCTTCTCCAGTTAGGTTTGTCTTTTGAACAAAAGATAACAAATACCAAGGTATGGCAAGTTGTGAAGACAGCAT
 TAAACATACCTAATTCACAGTATCTCTGTCCACACAGATGTTAGTATTATCTCTTTGAATCATTTGCTCAATAA
 TAAATATCCACCTTTCTCTGTATATCACAGGAAGTGAATTTGCAATTTTCTCAGTTCACTGTACTTATGTTACAGAA
 CCGTATCAGCGACCAAGAAATAGGACTGTGAGAGCTGCCAGTTATTACTGAACCATTAATACTTATATACTAAGAA
 TAAATAAATATATCCATGTGAAATATATATGGATTATGGATAACAAAGAGAGTGAAGGCCAAGCACTTTCTGTCTAC
 TGTACTCTTCTAAATGGAAATTTTAAAGTCACTAGCTGGCTTTACGTGTGTCTATTATTAGCAATTATTAATATGATGAT
 AGTATAATCCAGTAAGTGTGAAGAAATGTTTACTTAAAGAGGGATTTTCTTTTAAAGTCTGAATAAGTCTACTG
 GAAGAATTATCTCTCTGGGTGAAAAAGCTTTTGTGTGTCTTATTTTTAAATAACCGGAGTCAATTTATTAATGTT
 CTTGAAGTACTATTCCAGGGATTTTATGACACAAACCATATTGTGACAGAGATGAGCCTCTGTACTGTAAATAAGA
 AATGAAGTAGAGAAATGTTAAATATTTATGAGTTTACATATATAGTAAATAAAGGCTGATGTAAATGAATGCTGCACAA
 ACGGTGTCTATGATATCTTTTAGTAGTACTTTAGGAAAACTACACATTCTCAGAGGCTCTTGATGTCTCTAATGAAGGG
 GGGGAATGCTCTAATGAGAACAGTCAAAATTTTAGCATATAATTACAAGACAGCCTGTGGATATGATCATTAA
 TGATTTTGTGTGATCTGTGCCATTGCTTTTTTATTTAAAGAAATTTTGTAAATTAATGCCCTTTTCTAAAAAAA

FIG. 24b

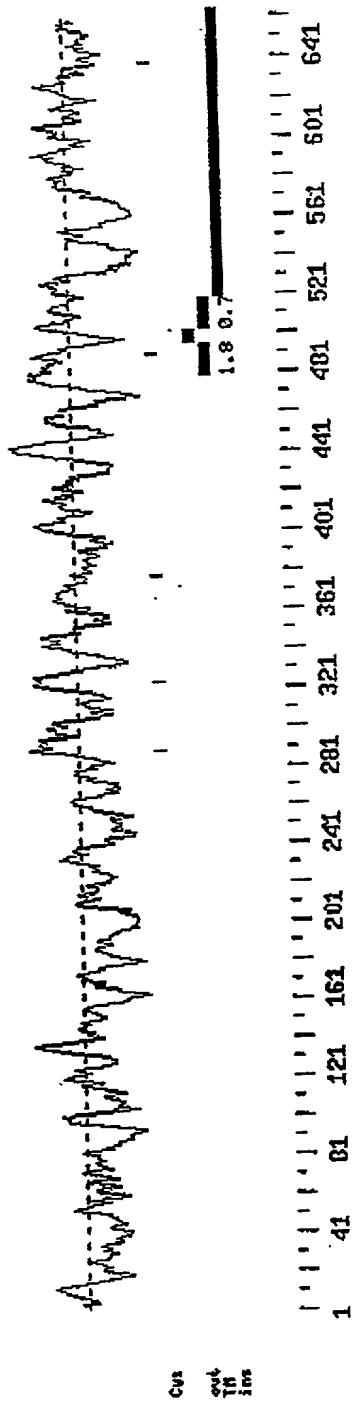


FIG. 25

```

*->PiivekcveyleklyPLaerGlqeEGYRvsGsa...srvkeLrea SEQ ID NO:32
P+i +k+++ Ie+ rGl++EG+ R++G a + +++++eL ++
33425 343 PLIFQKLISRIEE-----RGLTEGLLRIPGAAirikNLCQELEAK 383

fdkdgapdslelsekewfdvhvvagllKlYlReLPePLipydlyeefira
f ++ + + e+ ++ h a+llKl++ReLP+PL++ + + f
33425 384 FYEG--TFNWESVKQ----HDAASLLKLFIRELPQPLLSVEYLKAFQAV 426

akeqiedpderlralkellsSkLPrahynTLryLltHlnrvaeiyiensa
+ ++ ++l+al+ l+ +LE+a+++Tl++Ll++L+rv+ n +
33425 427 QN--LPTKKQQLQALNLLVI--LLPDANRDTLKALLEFLQRVID---NKE 469

vNkMnarNLAivFgPtLlirppdkesnd<-*
+NKM++ N A v +P+L+ + ++
33425 470 KNKMTVMNVAMVMAPNLFMCHA--LGL 494

```

FIG. 26

```

Query: 516 IKYQKLLWTIPKFIVNQVRKQNTENHXXXXXX--XXXXXXXXXXYDREK-----YEKQ 565
+KYQK+LW +P F++ QVR+ N +RE +K
Sbjct: 1 LKYQKILWKVPSFLITQVRMNEATMLLKKQLPSVRKLLRRKTLERETASPKTSKVLQKS 60 SEQ ID NO:33

Query: 566 DKSTNDADVPOGVIRVQAPHL SKVSMAIQLTEELKASDVLARF 608
+ +DVP+GVIRV AP LSKVSMAIQL + KA D+LA+F
Sbjct: 61 PSARRMSDVPEGVIRVHAPLLSKVSMAIQLNNQTKAKDILAKF 103

```

FIG. 27

```

Query: 390 NWESVKQ-HDAASLLKLFIRELPQPLLSVE----YLKAFQA-VQNLPTKXXXXXXXXXX 443
N E + H A LLK + RELP+PLL+ E +++A +A V + +
Sbjct: 16 NMEEYEDVHTVAGLLKQYFRELPEPLLTYELYEEFIEAQAQVSEDERMEALEMLKELI 75 SEQ ID NO:34

Query: 444 XXXPDANRDTLKALLEFLQRVIDNKEKNKMTVMNVAMVMAPNL 486
P+ANR+TL+ LL+ L RV + E+NKM N+A+V P L
Sbjct: 76 KLLPEANRETLYLLKHLRVAQHSEENKMNAQNLAUVFGPTL 118

```

FIG. 28

Query: 399 AASLLKLFIRELPQPLLSEVYLKAFQAVQNLPKKXXXXXXXXXXXXXXXXPDANRDTLKALL 458
A SLLKLF+REL P+PLL+ + + F+ V + P P NR L +L
Sbjct: 96 ACSLLKLFLERELPEPLLTDLVARFEEVASHPKVTTQQAELQQLLEQLPKNRTLLAWVL 155 SEQ ID NO:35

Query: 459 EFLQRVIDNKEKNKMTVMNVAMVMAFNLFM 488
VI + NK+ ++AM+++P L M
Sbjct: 156 LHFDAVITQQRHNKLNQSLAMLLSEPTLQM 185

FIG. 29